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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=11; day=24; hr=10; min=49; sec=29; ms=158; ]

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\*\*\*\*\*

Reviewer Comments:

<160> 9

<170> KopatentIn 1.71

The number provided for numeric identifier <160> must match the total number of sequences in the file. There are 11 sequences in this sequence listing but, 9 is given as the total in numeric identifier <160>, "<160> 9." Please make all necessary changes.

<210> 5

<211> 68

<212> PRT

<213> Artificial Sequence

<400> 5

For all sequences using "Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is made in the laboratory, please indicate that the sequence is synthesized. These errors appear in other sequences in the sequence listing. Please make all necessary changes.

\*\*\*\*\*

Application No: 10593413 Version No: 1.0

Input Set:

Output Set:

**Started:** 2008-10-28 16:16:48.335  
**Finished:** 2008-10-28 16:16:52.980  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 645 ms  
**Total Warnings:** 9  
**Total Errors:** 34  
**No. of SeqIDs Defined:** 9  
**Actual SeqID Count:** 11

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E 300	Invalid codon found Gly SEQID (8) POS: 337
E 300	Invalid codon found Gly SEQID (8) POS: 340
E 300	Invalid codon found Ser SEQID (8) POS: 343
E 300	Invalid codon found Ser SEQID (8) POS: 346
E 300	Invalid codon found Ser SEQID (8) POS: 349
E 300	Invalid codon found Gly SEQID (8) POS: 352
E 300	Invalid codon found Thr SEQID (8) POS: 355
E 300	Invalid codon found Val SEQID (8) POS: 358

**Input Set:**

**Output Set:**

**Started:** 2008-10-28 16:16:48.335

**Finished:** 2008-10-28 16:16:52.980

**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 645 ms

**Total Warnings:** 9

**Total Errors:** 34

**No. of SeqIDs Defined:** 9

**Actual SeqID Count:** 11

Error code	Error Description
E 300	Invalid codon found Asn SEQID (8) POS: 361
E 300	Invalid codon found Pro SEQID (8) POS: 364
E 300	Invalid codon found Val SEQID (8) POS: 367
E 300	Invalid codon found Pro SEQID (8) POS: 370
E 300	Invalid codon found Thr SEQID (8) POS: 373
E 300	Invalid codon found Thr SEQID (8) POS: 376
E 300	Invalid codon found Ala SEQID (8) POS: 379
E 300	Invalid codon found Ser SEQID (8) POS: 382
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (337)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (343)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (352)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (358)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (367)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (373)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)

**Input Set:**

**Output Set:**

**Started:** 2008-10-28 16:16:48.335  
**Finished:** 2008-10-28 16:16:52.980  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 645 ms  
**Total Warnings:** 9  
**Total Errors:** 34  
**No. of SeqIDs Defined:** 9  
**Actual SeqID Count:** 11

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 252	Calc# of Seq. differs from actual; 9 seqIds defined; count=11

## Sequence Listing

<110> SJ BIOMED INC.

<120> Anti-obese immunogenic hybrid polypeptides and anti-obese vaccine composition comprising the same

<160> 9

<170> KopatentIn 1.71

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> mimetic peptide for apolipoprotein B-100 epitope

<400> 1

Arg	Asn	Val	Pro	Pro	Ile	Phe	Asn	Asp	Val	Tyr	Trp	Ile	Ala	Phe
1				5					10					15

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> mimetic peptide for apolipoprotein B-100 epitope

<400> 2

Arg	Phe	Arg	Gly	Leu	Ile	Ser	Leu	Ser	Gln	Val	Tyr	Leu	Asp	Pro
1				5					10					15

<210> 3

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> mimetic peptide for apolipoprotein B-100 epitope

<400> 3

Ser	Val	Cys	Gly	Cys	Pro	Val	Gly	His	His	Asp	Val	Val	Gly	Leu
1				5					10					15

<210> 4

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence for terameric mimetic peptide

<220>

<221> CDS

<222> (1)..(204)

<400> 4

gtc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att gca 48  
Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala  
1 5 10 15

ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att 96  
Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile  
20 25 30

gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg 144  
Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp  
35 40 45

att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat 192  
Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr  
50 55 60

tgg att gca ttc 204  
Trp Ile Ala Phe  
65

<210> 5

<211> 68

<212> PRT

<213> Artificial Sequence

<400> 5

Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala  
1 5 10 15

Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile  
20 25 30

Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp  
35 40 45

Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr  
50 55 60

Trp Ile Ala Phe  
65

<210> 6

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<211>      180
<212>      DNA
<213>      Hepatitis B virus

<220>
<221>      CDS
<222>      (1)..(177)
<223>      Hepatitis B virus pres2

<220>
<221>      terminator
<222>      (178)..(180)

<400>      6
atg cag tgg aac tcc acc aca ttc cac caa gct ctg cta gat ccc aga      48
Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg
   1             5             10             15

gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt tcc gga aca gta      96
Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
      20             25             30

aac cct gtt ccg act act gcc tca ccc ata tcg tca atc ttc tcg agg      144
Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg
      35             40             45

act ggg gac cct gca ccg aac ctc gag cgg tca          taa          180
Thr Gly Asp Pro Ala Pro Asn Leu Glu Arg Ser
   10             55

<210>      7
<211>      59
<212>      PRT
<213>      Hepatitis B virus

<400>      7
Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg

   1             5             10             15
Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
      20             25             30

Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg
      35             40             45

Thr Gly Asp Pro Ala Pro Asn Leu Glu Arg Ser
   10             55

<210>      8
<211>      444
<212>      DNA
<213>      Artificial Sequence

<220>

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<223> DNA sequence for hybride polypeptide

<220>

<221> CDS

<222> (1)..(441)

<220>

<221> terminator

<222> (441)..(444)

<400> 8

atg aga gga tcg cat cac cat cac cat cac gga tcc gat gat gat gac	48
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp	
1 5 10 15	
aag atc gtc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg	96
Lys Ile Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp	
20 25 30	
att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat	144
Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr	
35 40 45	
tgg att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt	192
Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val	
50 55 60	
tat tgg att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat	240
Tyr Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp	
65 70 75 80	
gtt tat tgg att gca ttc ctc gac atg cag tgg aac tcc acc aca ttc	288
Val Tyr Trp Ile Ala Phe Leu Asp Met Gln Trp Asn Ser Thr Thr Phe	
85 90 95	
cac caa gct ctg cta gat ccc aga gtg agg ggc cta tat ttt cct gct	336
His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala	
100 105 110	
ggg ggc tcc agt tcc gga aca gta aac cct gtt ccg act act gcc tca	384
Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser	
115 120 125	
ccc ata tcg tca atc ttc tcg agg act ggg gac cct gca ccg aac ctc	432
Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Leu	
130 135 140	
gag cgg tca taa	444
Glu Arg Ser	
145	

<210> 9

<211> 147

<212> PRT  
 <213> Artificial Sequence

<400> 9  
 Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp  
 1 5 10 15  
 Lys Ile Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp  
 20 25 30  
 Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr  
 35 40 45  
 Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val  
 50 55 60  
 Tyr Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp  
 65 70 75 80  
 Val Tyr Trp Ile Ala Phe Leu Asp Met Gln Trp Asn Ser Thr Thr Phe  
 85 90 95  
 His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala  
 100 105 110  
 Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser  
 115 120 125  
 Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Leu  
 130 135 140  
 Glu Arg Ser  
 145

<210> 10  
 <211> 432  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> DNA sequence for PTB14

<220>  
 <221> CDS  
 <222> (1)..(429)

<400> 10  
 atg aga gga tcg cat cac cat cac cat cac gga tcc gat gat gat gac 48  
 Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp  
 1 5 10 15  
 aag atc gtc gac atg cag tgg aac tcc acc aca ttc cac caa gct ctg 96  
 Lys Ile Val Asp Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu

20	25	30	
cta gat ccc aga gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt			144
Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser			
35	40	45	
tcc gga aca gta aac cct gtt ccg act act gcc tca ccc ata tcg tca			192
Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser			
50	55	60	
atc ttc tcg aag act ggg gac cct gca ccg aac ctc gac cgt aat gtt			240
Ile Phe Ser Lys Thr Gly Asp Pro Ala Pro Asn Leu Asp Arg Asn Val			
65	70	75	80
cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac cgt aat			288
Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg Asn			
85	90	95	
gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac cgt			336
Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg			
100	105	110	
aat gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac			384
Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp			
115	120	125	
cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc			430
Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe			
130	135	140	
aa			432

<210> 11  
 <211> 143  
 <212> PRT  
 <213> Artificial Sequence

<400> 11  
 Met Arg Gly Ser His His His His His Gly Ser Asp Asp Asp Asp  
 1 5 10 15  
 Lys Ile Val Asp Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu  
 20 25 30  
 Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser  
 35 40 45  
 Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser  
 50 55 60  
 Ile Phe Ser Lys Thr Gly Asp Pro Ala Pro Asn Leu Asp Arg Asn Val  
 65 70 75 80  
 Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg Asn

85

90

95

Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg  
100 105 110

Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp  
115 120 125

Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe  
130 135 140